AMENDMENTS

IN THE CLAIMS

1. -- 68. (Canceled).

69. **(Currently Amended)** A method for determining the identity of a polymorphic nucleotide in a target sequence having at least two known variant nucleotides at a site, comprising:

performing a primer extension reaction with the target sequence using an extension reaction mixture comprising:

a primer that specifically hybridizes to the target sequence such that **there is a one or more nucleotide gap between** the 3' **terminus** ~~end~~ of the primer **and** ~~is one or more~~ nucleotides ~~5' of a~~ **the** variant nucleotide **of the polymorphic site of the target sequence** ~~at the polymorphic site~~, and

a mixture of ~~a plurality of~~ deoxyribonucleoside triphosphates (dNTPs) or ribonucleoside triphosphates (rNTPs), where the ~~plurality~~ **mixture** of dNTPs or rNTPs provide**s** for at least one nucleotide extension of the primer when hybridized to a target sequence having either of the two variant nucleotides at the polymorphic site, wherein the mixture excludes a dNTP or rNTP complementary to one of said variant nucleotides of the polymorphic site, **and** wherein the dNTPs or rNTPs in the mixture are not detectably labeled or modified, and

wherein the extension reaction is performed in the absence of a dideoxynucleoside triphosphate (ddNTP); and

analyzing ~~reaction~~ **primer extension** products of said extension reaction;

wherein the length of the primer extension products is indicative of the identity of the variant nucleotides at the polymorphic site.

70. **(Canceled)**

71. **(Currently Amended)** The method of claim 69, wherein the primer hybridizes to the target sequence such that **there is a gap of at least two nucleotides between the 3' terminus of the primer**

and the variant nucleotide of the polymorphic of the target sequence ~~its 3' end is 2 or more nucleotides 5' of the variant nucleotide~~.

72. **(Previously Added)** The method of claim 69, wherein said analyzing comprises determining the length of said reaction products.

73. **(Previously Added)** The method of claim 69, wherein said analyzing comprises performing a technique selected from the group consisting of chromatography, capillary electrophoresis, microfluidic analysis, and slab gel electrophoresis.

74. **(Previously Added)** The method of claim 69, wherein said analyzing comprises performing high performance liquid chromatography.

75. **(Previously Added)** The method of claim 69, wherein said analyzing comprises performing capillary electrophoresis.

76. **(Previously Added)** The method of claim 69, wherein said analyzing reaction products comprises determining the identity of a nucleotide incorporated in a reaction product.

77. **(Previously Added)** The method of claim 69, wherein said analyzing comprises use of an intercalating agent.

78. **(Previously Added)** The method of claim 77, wherein the intercalating agent is ethidium bromide.

79. **(Previously Added)** The method of claim 77, wherein the intercalating agent is an unsymmetrical cyanine dye.

80. **(Previously Added)** The method of claim 69, wherein said analyzing comprises use of slab electrophoresis and ultraviolet light.

81. **(Previously Added)** The method of claim 69, wherein the reaction products are detected using slab electrophoresis and a DNA-binding dye.

82. **(Previously Added)** The method of claim 69, wherein the target sequence comprises a biallelic marker associated with genetic disorders.

83. **(Previously Added)** The method of claim 69, wherein the target sequence is present in a sample obtained from a diploid organism.

84. **(Currently Amended)** A method for screening a DNA sample for a plurality of target sequences having at least two known variants, comprising:

contacting a sample comprising a plurality of known target sequences with an extension reaction mixture **to produce primer extension reaction products**, the **extension reaction** mixture comprising

a primer that specifically hybridizes to a target sequence of interest such that **there is a one or more nucleotide gap between** the 3' ~~end~~ **terminus** of the primer **and** ~~is at least one nucleotide 5' of a~~ **the** variant nucleotide of the polymorphic site **of the target sequence**, and

a ~~plurality~~ **mixture** of deoxyribonucleoside triphosphates (dNTPs) or ribonucleoside triphosphates (rNTPs), where the ~~plurality of~~ dNTPs or rNTPs **in the mixture** provide for at least one nucleotide extension of the primer when hybridized to a target sequence having either of the two variant nucleotides, the mixture excluding a dideoxynucleoside triphosphate (ddNTP) and further excluding a dNTP or rNTP complementary to one of said variant nucleotides of the SNP, wherein the dNTPs or rNTPs in the mixture are not detectably labeled or modified; and

analyzing the ~~reaction~~ **primer extension** products ~~of each extension reaction;~~

wherein the length of the primer extension products is indicative of the identity of the variant nucleotides at the polymorphic site.

85. **(Previously Added)** The method of claim 84, wherein the target sequence is associated with genetic disorders.

86. **(Previously Added)** The method of claim 84, wherein the sample is from a diploid organism.

87. **(Currently Amended)** The method of claims 84, wherein the extension reaction mixture comprises **at least two** ~~a plurality of~~ different primers, which primers specifically hybridize to different target sequences, wherein each primer is of a length or sequence such that extension products of the different primers can be distinguished one from another.

88. **(Previously Added)** The method of claim 87, wherein the different primers are of different lengths.